



OIPE

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/729,141B

TIME: 12:05:25

Input Set : A:\sequence listing 09729141.txt

Output Set: N:\CRF4\04032003\I729141B.raw

4 <110> APPLICANT: Logemann, Juergen
 5 Jach, Guido
 6 Gornhardt, Birgit
 7 Mundy, John
 8 Schell, Jeff
 9 Eckes, Peter
 10 Chet, Ilan
 12 <120> TITLE OF INVENTION: Transgenic pathogen-resistant organism
 15 <130> FILE REFERENCE: A29542-FWC-I-R 070037.0195
 17 <140> CURRENT APPLICATION NUMBER: US 09/729,141B
 C--> 18 <141> CURRENT FILING DATE: 2003-03-25
 20 <150> PRIOR APPLICATION NUMBER: 08/812,025
 21 <151> PRIOR FILING DATE: 1997-03-06
 23 <150> PRIOR APPLICATION NUMBER: 08/457,797
 24 <151> PRIOR FILING DATE: 1995-06-01
 26 <150> PRIOR APPLICATION NUMBER: 08/134,416
 27 <151> PRIOR FILING DATE: 1993-10-08
 29 <160> NUMBER OF SEQ ID NOS: 12
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 275
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Aspergillus giganteus
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (46)...(225)
 42 <400> SEQUENCE: 1
 43 ttgccacccc cggtgaagcc gattctctca ccgctggtgg tctgg atg caa gag atg 57
 44 Met Gln Glu Met
 45 1
 47 aga gcg cgg gtt ttg gcc aca tac aat ggc aaa tgc tac aag aag gat 105
 48 Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp
 49 5 10 15 20
 51 aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag 153
 52 Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys
 53 25 30 35
 55 tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac 201
 56 Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp
 57 40 45 50
 59 agc tac aag ggg aag tgc tac tgc tagacggtga gcgaaggac gaagtaggct 255
 60 Ser Tyr Lys Gly Lys Cys Tyr Cys
 61 55 60
 63 ggggggttatt ttactctgct 275

ENTERED

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/729,141B

TIME: 12:05:25

Input Set : A:\sequence listing 09729141.txt

Output Set: N:\CRF4\04032003\I729141B.raw

```

65 <210> SEQ ID NO: 2
66 <211> LENGTH: 60
67 <212> TYPE: PRT
68 <213> ORGANISM: Aspergillus giganteus
70 <400> SEQUENCE: 2
71 Met Gln Glu Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys
72 1          5          10          15
73 Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr
74          20          25          30
75 Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys
76          35          40          45
77 Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys
78 50          55          60
81 <210> SEQ ID NO: 3
82 <211> LENGTH: 51
83 <212> TYPE: PRT
84 <213> ORGANISM: Aspergillus giganteus
86 <400> SEQUENCE: 3
87 Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp Asn Ile Cys Lys Tyr
88 1          5          10          15
89 Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys Cys Tyr Val Lys Lys
90          20          25          30
91 Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys
92          35          40          45
93 Cys Tyr Cys
94 50
97 <210> SEQ ID NO: 4
98 <211> LENGTH: 1032
99 <212> TYPE: DNA
100 <213> ORGANISM: Hordeum vulgare
102 <220> FEATURE:
103 <221> NAME/KEY: 5'UTR
104 <222> LOCATION: (1)...(42)
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (43)...(885)
W--> 109 <221> 3'UTR
110 <222> LOCATION: (886)...(1032)
111 <223> OTHER INFORMATION: 46 nucleotides at the 3' end not shown
W--> 113 <221> polyA_signal
114 <222> LOCATION: (930)...(935)
115 <223> OTHER INFORMATION: potential polyadenylation signal
W--> 117 <221> polyA_signal
118 <222> LOCATION: (963)...(976)
119 <223> OTHER INFORMATION: potential polyadenylation signal
W--> 121 <221> polyA_signal
122 <222> LOCATION: (1002)...(1011)
123 <223> OTHER INFORMATION: potential polyadenylation signal
W--> 125 <221> mat_peptide
126 <222> LOCATION: (46)...(886)

```

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/729,141B

TIME: 12:05:25

Input Set : A:\sequence listing 09729141.txt

Output Set: N:\CRF4\04032003\I729141B.raw

W--> 128 <400> 4

```

129 cttaatagca catcttgtcc gtcttagctt tgcattacat cc atg gcg gca aag      54
130                                     Met Ala Ala Lys
131                                     1
133 atg gcg aag aac gtg gac aag ccg ctc ttc acc gcg acg ttc aac gtc      102
134 Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val
135 5 10 15 20
137 cag gcc agc tcc gcc gac tac gcc acc ttc atc gcc ggc atc cgc aac      150
138 Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn
139 25 30 35
141 aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg      198
142 Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro
143 40 45 50
145 ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc      246
146 Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu
147 55 60 65
149 aag gcc tcg ccg acc agc gcc ggg ctc acg ctg gcc att cgg gcg gac      294
150 Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp
151 70 75 80
153 aac atc tac ctg gag ggc ttc aag agc agc gac ggc acc tgg tgg gag      342
154 Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly Thr Trp Trp Glu
155 85 90 95 100
157 ctc acc ccg ggc ctc atc ccc ggc gcc acc tac gtc ggg ttc ggc ggc      390
158 Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val Gly Phe Gly Gly
159 105 110 115
161 acc tac cgc gac ctc ctc ggc gac acc gac aag ctg acc aac gtc gct      438
162 Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu Thr Asn Val Ala
163 120 125 130
165 ctc ggc cgg cag cag ctg gcg gac gcg gtg acc gcc ctc cac ggg cgc      486
166 Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala Leu His Gly Arg
167 135 140 145
169 acc aag gcc gac aag ccg tcc ggc ccg aag cag cag cag gcg agg gag      534
170 Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln Gln Ala Arg Glu
171 150 155 160
173 gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acg cgg ttc cag      582
174 Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln
175 165 170 175 180
177 acg gtg tct ggg ttc gtg gcc ggg ttg ctg cac ccc aag gcg gtg gag      630
178 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu
179 185 190 195
181 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg      678
182 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
183 200 205 210
185 tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag cct ccg      726
186 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
187 215 220 225
189 ccg gga aag tcg cca gcg aag ttc gcg ccg atc gag aag atg ggc gtg      774
190 Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu Lys Met Gly Val
191 230 235 240

```

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/729,141B

TIME: 12:05:25

Input Set : A:\sequence listing 09729141.txt

Output Set: N:\CRF4\04032003\I729141B.raw

```

193 agg acg gct gta cag gcc gcc aac acg ctg ggg atc ctg ctg ttc gtg 822
194 Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile Leu Leu Phe Val
195 245 250 255 260
197 gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttc cat 870
198 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
199 265 270 275
201 gcg agt ggt ggg aaa taggtagttt tccaggtata cctgcatggg tagtgtaaaa 925
202 Ala Ser Gly Gly Lys
203 280
205 gtcgaataaaa catgtcacag agtgacggac tgatataaat aaataaataa acgtgtcaca 985
206 gagttacata taaacaaata aataaataat taaaaatgtc cagttta 1032
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 281
210 <212> TYPE: PRT
211 <213> ORGANISM: Hordeum vulgare
213 <400> SEQUENCE: 5
214 Met Ala Ala Lys Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala
215 1 5 10 15
216 Thr Phe Asn Val Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala
217 20 25 30
218 Gly Ile Arg Asn Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg
219 35 40 45
220 Pro Val Leu Pro Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe
221 50 55 60
222 His Val Val Leu Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala
223 65 70 75 80
224 Ile Arg Ala Asp Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly
225 85 90 95
226 Thr Trp Trp Glu Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val
227 100 105 110
228 Gly Phe Gly Gly Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu
229 115 120 125
230 Thr Asn Val Ala Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala
231 130 135 140
232 Leu His Gly Arg Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln
233 145 150 155 160
234 Gln Ala Arg Glu Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala
235 165 170 175
236 Thr Arg Phe Gln Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro
237 180 185 190
238 Lys Ala Val Glu Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala
239 195 200 205
240 Gln Val Asn Gly Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp
241 210 215 220
242 Val Lys Pro Pro Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu
243 225 230 235 240
244 Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile
245 245 250 255
246 Leu Leu Phe Val Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu

```

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/729,141B

TIME: 12:05:25

Input Set : A:\sequence listing 09729141.txt

Output Set: N:\CRF4\04032003\I729141B.raw

```

247          260          265          270
248 Glu Leu Phe His Ala Ser Gly Gly Lys
249          275          280
252 <210> SEQ ID NO: 6
253 <211> LENGTH: 480
254 <212> TYPE: DNA
255 <213> ORGANISM: Hordeum vulgare
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (1)...(351)
260 <223> OTHER INFORMATION: protein syntheis inhibitor (PSI), aminoterminally
261      incomplete protein from an incomplete PSI cDNA
262      clone
264 <221> NAME/KEY: 3'UTR
W--> 265 <222> LOCATION: (352)...(487)
W--> 267 <221> polyA_signal
W--> 268 <222> LOCATION: (404)...(409)
      269 <223> OTHER INFORMATION: potential polyadenylation signal
W--> 271 <221> polyA_signal
W--> 272 <222> LOCATION: (437)...(442)
      273 <223> OTHER INFORMATION: potential polyadenylation signal
W--> 275 <221> polyA_signal
W--> 276 <222> LOCATION: (445)...(450)
      277 <223> OTHER INFORMATION: potential polyadenylation signal
W--> 279 <400> 6
280 gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acg cgg ttc cag 48
281 Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln
282 1          5          10          15
284 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96
285 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu
286          20          25          30
288 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144
289 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
290          35          40          45
292 tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag ccc ccg 192
293 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
294          50          55          60
296 ccg gga aag tcg cca gcg aag ttc acg ccg atc gag aag atg ggc gtg 240
297 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
298 65          70          75          80
300 agg act gct gag cag gct gcg gct act ttg ggg atc ctg ctg ttc gtt 288
301 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
302          85          90          95
304 gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336
305 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
306          100          105          110
308 gcg agt ggt ggg aaa taggtagttt tgcaggtata cctgcatggg taaatgtaaa 391
309 Ala Ser Gly Gly Lys
310          115

```

VERIFICATION SUMMARY

DATE: 04/03/2003

PATENT APPLICATION: US/09/729,141B

TIME: 12:05:26

Input Set : A:\sequence listing 09729141.txt

Output Set: N:\CRF4\04032003\I729141B.raw

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:113 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:117 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:121 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:125 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:265 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, 3UTR LOCATION: (352)...
(487)
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:271 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:275 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:279 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:403 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:407 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:411 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:415 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:419 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:423 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:427 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:431 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:434 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:563 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:567 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:571 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:575 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:578 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11